

Amendments to the Specification:

Please replace paragraph [24] with the following amended paragraph:

--[24] The present invention also provides polynucleotide microarrays. In some embodiments, the polynucleotide microarrays hybridize to first and a second labeled DNA portions, wherein the portions are from uniformly-sized populations of randomly cleaved or sheared DNA from a cell, tissue, or organism; wherein the first DNA portion comprises unmethylated and methylated DNA labeled with a first label; and wherein the second DNA portion is depleted for either unmethylated DNA or methylated DNA and the second portion of DNA is labeled with a second label different from the first label. --

Please replace paragraph [73] with the following amended paragraph:

--[73] In some embodiments, the organism is a plant. In some embodiments, the organism is a fungus. In some embodiments, the organism is a prokaryote. In some embodiments, the prokaryote is a bacterial pathogen. In some embodiments, the bacterial pathogen is selected from the group consisting of gram negative and gram positive species, which include *Listeria*, *E. coli*, *Salmonella*, *Yersinia*, and *Neisseria*, and mycobacteria. In some embodiments, the organism is an animal. In some embodiments, the animal is a human. ~~In some embodiments, the cell is a stem cell. In some embodiments, the cell is transgenic and the nucleic acid corresponds to the insertion site of a transgene.~~ In some embodiments, the cell is a stem cell. In some embodiments, the cell is transgenic and the nucleic acid corresponds to the insertion site of a transgene. In some embodiments, the tissue is blood. In some embodiments, the tissue is biopsy tissue. In some embodiments, the tissue is resected tissue. In some embodiments, the tissue is normal. In some embodiments, the tissue is tumor tissue. In some embodiments, the tissue is precancerous.--

Please replace paragraph [127] with the following amended paragraph:

--[127] In this application, genomic DNA from two different individuals, cell lines, or organisms, for example, are sheared or randomly cleaved to create uniformly-sized DNA fragments. A portion (e.g., half) of each sample is then digested with a methylation sensitive or methylation dependent enzyme, as described herein. All four samples are then refragmented to isolate total DNA and either methylated or unmethylated DNA ~~sub-portionss~~ sub-portions from each individual. These four samples can then be hybridized to a nucleic acid, e.g., a microarray. In some embodiments, the four samples are labeled with four different labels (e.g., fluorescent dyes). The ratio of total DNA samples provides the CGH profile, while the ratio of depleted and total samples provides the methylation profile from each individual.--